

# Resource Summary Report

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## MUMmer

RRID:SCR\_018171

Type: Tool

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### Proper Citation

MUMmer (RRID:SCR\_018171)

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### Resource Information

**URL:** <http://mummer.sourceforge.net/>

**Proper Citation:** MUMmer (RRID:SCR\_018171)

**Description:** Software package as system for rapidly aligning entire genomes. Alignment tool for DNA and protein sequences. Can align incomplete genomes.

**Synonyms:** MUMmer4, MUMmer 3.0

**Resource Type:** alignment software, data processing software, image analysis software, software application, software resource

**Defining Citation:** [PMID:14759262](#)

**Keywords:** Align, genome, DNA, protein, sequence, , bio.tools

**Funding:** NIAID N01 AI15447;  
NLM R01 LM06845;  
NSF IIS 9902923

**Availability:** Free, Available for download, Freely available

**Resource Name:** MUMmer

**Resource ID:** SCR\_018171

**Alternate IDs:** OMICS\_14554, biotools:mummer

**Alternate URLs:** <https://github.com/mummer4/mummer>, <https://bio.tools/mummer>,  
<https://sources.debian.org/src/mummer/>

**License:** Artistic License 2.0

**Record Creation Time:** 20220129T080339+0000

## Ratings and Alerts

No rating or validation information has been found for MUMmer.

No alerts have been found for MUMmer.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 547 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [NIF](#) .

Dong W, et al. (2026) PHR-Mediated Pi Starvation Response Mobile Messenger RNAs Represent Noncoding Transcripts in Recipient Tissues. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(4), e02911.

Yang D, et al. (2026) Global genomic landscape of *Staphylococcus lugdunensis*: population structure, antimicrobial resistance, and virulence determinants. *Applied and environmental microbiology*, 92(3), e0189325.

Qi H, et al. (2026) Emergence of blaNDM-5 and international dissemination of an ST26 *Salmonella* Thompson resistance gene-enriched sublineage. *BMC microbiology*, 26(1).

Xie Z, et al. (2026) Susceptibility of *Candida auris* isolates to antifungal agents: perspectives from whole-genome sequencing and phenotypic testing. *BMC microbiology*, 26(1).

Wang H, et al. (2026) Integrative chloroplast genomics of Polygonaceae: evolutionary dynamics, codon optimization, and phylogenetic resolution. *BMC plant biology*, 26(1).

Chen N, et al. (2026) A Chromosome-Level Genome Assembly and Annotation of the Chinese Porcupine (*Hystrix hodgsoni*) Reveals the Expansion of Olfactory-Related Gene Families. *Genes*, 17(6).

Liang M, et al. (2026) IVCDB: a comprehensive database of iridoviruses for epidemiology, genetic evolution, and disease management. *Nucleic acids research*, 54(D1), D790.

Wang J, et al. (2026) Exploring differences in the human gut microbiome between Han Chinese and non-Chinese populations. *Genome biology*, 27(1), 34.

Mao X, et al. (2026) Sex chromosome evolution mediated by a large inversion and a possible switch of the sex determination gene. *Genome biology*, 27(1).

- Li T, et al. (2026) Assembly and comparative analysis of the complete multichromosomal mitochondrial genome of an endangered orchid species, *Calanthe sieboldii*. *Frontiers in plant science*, 17, 1701753.
- Dumetz F, et al. (2026) The UTRs of *Leishmania donovani* vary in length and are enriched in potential regulatory structures. *PLoS pathogens*, 22(3), e1013551.
- Chen W, et al. (2026) A near telomere-to-telomere genome assembly of *Pterocryptis cochinchinensis*. *Scientific data*, 13(1).
- Lee YY, et al. (2026) Establishment of a congenic strain for the oyster mushroom reveals the structure and evolution of mating-type loci. *PLoS genetics*, 22(4), e1011966.
- Tsiouri O, et al. (2026) Comparative analysis towards the identification of genome wide characteristics of a beneficial fungal endophyte. *Scientific reports*, 16(1).
- Luo X, et al. (2026) Comprehensive genomic analysis of carbapenem-resistant *Citrobacter freundii* and characterization of a co-carrying blaKPC-2 and blaNDM-1 isolate in Zhejiang Province???. *BMC microbiology*, 26(1).
- Pezzi PH, et al. (2026) Chromosome-Level Reference Genome of the Beach False Foxglove, *Agalinis fasciculata* (Orobanchaceae). *Genome biology and evolution*, 18(5).
- Zheng C, et al. (2026) Biological characteristics and genetics differentiation of smut fungi in *Coix L*. *Frontiers in microbiology*, 17, 1746178.
- Pantoja L, et al. (2026) Genomic Analysis of Gut Bacteria in *Tecia Solanivora*: Insights into Host Functions and Their Potential in Biocontrol. *Current microbiology*, 83(8).
- Hunt M, et al. (2026) Addressing pandemic-wide systematic errors in the SARS-CoV-2 phylogeny. *Nature methods*, 23(3), 653.
- Liu J, et al. (2026) Zoonotic *Bordetella bronchiseptica* infection at the swine-human interface: unveiling the evolutionary path from an animal to a human pathogen. *Emerging microbes & infections*, 15(1), 2637286.